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ALIGNMENTS

RESULT	1	CELCEDD3A	7653 bp	DNA	INV	23-FEB-1994
LOCUS		Caenorhabditis elegans	cell death protein (ced-3)	gene, complete		
DEFINITION		cds .				
ACCESSION	L29052					
NID	9456416					
VERSION	L29052.1	G1:456416	cell death Protein; interleukin-1 beta converting enzyme.			
KEYWORDS		Caenorhabditis elegans (strain N2) DNA.				
SOURCE		Caenorhabditis elegans				
ORGANISM		Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidae; Rhabditidae; Caenorhabditids.				
REFERENCE	1	(bases 1 to 7653)				
AUTHORS	Yuan,J., Shaham,S., Ledoux,S., Ellis,H.M. and Horvitz,H.					
TITLE	The C. elegans cell death gene ced-3 encodes a protein similar to mammalian interleukin-1b-converting enzyme					
JOURNAL	Cell 75, 641-652 (1993)					
MEDLINE	94061982					
FEATURES	Location/Qualifiers					

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RESULT	REFEREN
LOCUS	AUTHO
DEFINIT	TITLE
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VERSION	FEATURE
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Post-processing: Minimum Match 0%
Searched: 646147 seqs, 1385953633 base

Listing first 45 summaries

Statistics: Mean 11.336; Variance 8.769; scale 1.293
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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exon

534

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52

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Qy 4501 GCCTCATATCAATAATGACRCACTTGAGCAGATGCCAACCGGAATGGTACCAAGGGCG 4560

Db 4561 ACAGAGCANTCTTACCAATTTCTGAGTCATGGTATACGGTATTCGAGGACA 4520

Qy 4561 ACAGAGCANTCTTACCAATTTCTGAGTCATGGTATACGGTATTCGAGGACA 4620

Db 4621 ATCTGACGGAAAGGTACGGAAATTATACCCAAAGGAAATTGGTACGGTATTCGG 4680

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DEFINITION						
ACCESSION						
NID						
VERSION						
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SOURCE						
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AUTHORS						
TITLE						
JOURNAL						

Submitted (21-Oct-1996) Louis, MO 63110, USA. E-mail: jes@zanger.ac.uk or rwenematode.wustl.edu

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Cp 7429 ATGGATCCGGCAAAAT 7411

RESULT 10 LOCUS SCU43503 DEFINITION 38590 bp DNA ACCESSION U43303_00094 NID 91163087 VERSION 1
KEYWORDS Schizosaccharomyces pombe C18B11.10 homolog; NIP29; Aspergillus oryzae ribonuclease P2 homolog; ME15; *H. sapiens* G1197 EST homolog; DEP1; *S. kluuyveri* kORF1 homolog; ID11; *C. elegans* CEFL3G6.4 product homolog; BEM3; *E. coli* 2-hydroxyacid dehydrogenase homolog; tRNA_{met}

- CAR1; *S. cerevisiae* Pho81p homolog; Clostridium pasteurianum protein homolog.
Saccharomyces cerevisiae baker's yeast. Hemiascomycetes: Saccharomycetales:
Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Hemiascomycetes.
REFERENCE 1 (bases 1 to 38590)
ORGANISM SOURCE
AUTHORS Sumrada,R.A. and Cooper,T.G.
TITLE Nucleotide sequence of the *Saccharomyces cerevisiae* arginase gene (CAR1) and its transcription under various physiological conditions
JOURNAL J. Bacteriol. 160 (3), 1078-1087 (1984)
MEDLINE 85054621
REFERENCE 2 (bases 1 to 38590)
AUTHORS Anderson,M.S., Muehlbacher,M., Street,I.P., Proffitt,J. and Poulter,C.D.
TITLE Isopenetyl diphosphate:dimethylallyl diphosphate isomerase. An improved purification of the enzyme and isolation of the gene from *Saccharomyces cerevisiae*.
JOURNAL J. Biol. Chem. 264 (32), 19169-19175 (1989)
MEDLINE 90037050
REFERENCE 3 (bases 1 to 38590)
AUTHORS Jamieson,D.J. and Beggs,J.D.
TITLE A suppressor of yeast spp81/ded1 mutations encodes a very similar ATP-dependent RNA helicase
JOURNAL Mol. Microbiol. 5 (4), 805-812 (1991)
MEDLINE 91312117
REFERENCE 4 (bases 1 to 38590)
AUTHORS Zheng,Y., Cerione,R. and Bender,A.
TITLE Control of the yeast bud-site exchange by cdc24 and stimulation of Grp42, Catalysis guanine nucleotide exchange by cdc24 and stimulation of Grp42.
JOURNAL J. Biol. Chem. 269 (4), 2369-2372 (1994)
MEDLINE 94131990
REFERENCE 5 (bases 1 to 38590)
AUTHORS Bussey,H., Storms,R.K., Ahmed,A., Albermann,K., Allen,E., Benes,V., Botstein,D., Bowtell,B., Badcock,K., Barrell,B., Cherry,J.M., Chung,E., Churcher,C., Bruckner,M., Carpenter,J., Davis,R.W., Dietrich,F.S., Coster,F., Dusterhoff,R., Delius,H., DiPaolo,T., Dubois,E., Fritz,C., Duncan,M., Floeth,M., Fortin,N., Friesen,J.D., Hillier,L., Hunnicke-Smith,S., Hyman,R., Heumann,K., Heubling,J., Johnston,M., Kalman,S., Kleine,K., Komp,C., Kurdi,O., Lashkarai,D., Lewin,R., Lin,A., Louis,E.J., Marathe,R., Messenguy,F., Newes,R.W., Mirtiatti,S., Moestl,D., Muller,Auer,S., Namath,A., Neutze,W., Nentwich,U., Oefner,P., Pearson,D., Peter,F.X., Poli,T.M., Purnelle,D., Schafer,M., Scharfe,M., Scheeres,B., Schramm,S., Schroeder,M., Tettelin,H., Urrestarazu,L.A., Ushinsky,S., Vierendeels,F., Visser,S., Voss,H., Walsh,S.V., Wambutt,R., Wang,Y., Wedler,E., Wedler,H., Winnert,E., Zhong,W.W., Zoller,A., Vo,D.H. and Hani,J.
TITLE The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI
JOURNAL Nature 387 (6632 Suppl), 103-105 (1997)
MEDLINE 97313271
REFERENCE 6 (bases 1 to 38590)
AUTHORS Schiltenstedt,G. and Silver,P.A.
TITLE Unpublished
JOURNAL
REFERENCE 7 (bases 1 to 38590)
AUTHORS Hall,J., Ahmed,A., Bussey,H., Wang,Y. and Winnert,E.
TITLE The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm
JOURNAL
REFERENCE 8 (bases 1 to 38590)
AUTHORS Weber,L. and Byers,B.E.
TITLE me15, a novel melto mutation
JOURNAL
REFERENCE 9 (bases 1 to 38590)
AUTHORS Bussey,H.
TITLE Direct Submission
JOURNAL Sub205 Dr. Penfield Ave., Howard Bussey, McGill University, Biology, 1205 Dr. Penfield Ave., Montreal, Quebec H3A 1B1, Canada
REFERENCE 10 (bases 1 to 38590)
AUTHORS Jia,Y. and Cherry,J.M.
TITLE Direct Submission

JOURNAL Submitted (02-SEP-1997) Department of Genetics, Stanford University, Saccharomyces Genome Database, Stanford, CA 94305-5120, USA

COMMENT

Curated by:

Saccharomyces Genome Database

URL: <http://genome-www.stanford.edu/>

e-mail: yeast-curator@genome.stanford.edu

All CDS of 100 or more codons have been analyzed. CDS that are overlapped by larger CDS are not included. Cosmid 8209/8002 is overlapped at the beginning by cosmid 9545, and at the end by cosmid 8059.

FEATURES

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RESULTS

LOCUS HS657J8

DEFINITION Human DNA sequence from clone 657J8 on chromosome Xq26.1-16.3

ACCESSION AL034407

NID 93980437

VERSION AL034407.1

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 98954)

AUTHORS Graham,D.

TITLE Direct Submission

SUBMITTED (07-DEC-1998) Sanger Centre, Hinxton, Cambridge, UK

Query Match 4.2%

Score 19;

DB 28;

Length 38590;

Best Local Similarity 100.0%;

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Gaps 0;

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gene YPL123cp

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 Qy 4561 ACAGGACATCTTACCAATTGTCAGATGGCTATAACGGTTATTGCAAGGCCA 4620
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Db 4681 CGCAAATGTCGGCCGGCTCGACAGACAATTGTGTTAAATGCAAAATGTATAAT 4740
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RESULT 2
 LOCUS CEC48D1 39908 bp DNA INV
 DEFINITION Caenorhabditis elegans cosmid C48D1, complete sequence.
 ACCESSION 281049
 NID 91627677
 VERSION 781049.1 GI:1627677
 KEYWORDS HTG
 SOURCE Caenorhabditis elegans.
 ORGANISM Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;
 Caenorhabditis elegans.
 Rhabditina; Rhabditoidea; Rhabditidae; Peioderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 3908)
 AUTHORS Burton, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
 jesesanger.ac.uk or rwenemateode.wustl.edu

REFERENCE	AUTHORS	JOURNAL	FEATURES
DOCUMENT	MEDLINE	SOURCE	QUALIFIERS
2 (bases 1 to 39098)	Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Buron, J., Connell, N., Copsey, T., Cooper, J.J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latrell, P., Lightning, J., Lloyd, C., McMurry, B., O'Callaghan, M., Parsons, J., Percy, C., Riften, L., Roopra, A., Saunders, D., Shawkeen, R., Smaldo, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkison-Sprout, J. and Wholdman, P.	Nature 368 (6466), 32-38 (1994) 94150718	elegans 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
	Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.		
	For a graphical representation of this sequence and its analysis see:- http://webace.sanger.ac.uk/cgi-bin/display?db=wormbaseclass-Sequence&object=C48D1		
	Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subsections. Exceptions are indicated by an explicit note.		
	IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.		
	This sequence is the entire insert of clone C48D1. The true right end of clone F58D2 is at 18310 in this sequence. The start of this sequence (1..100) overlaps with the end of sequence 281093. The end of this sequence (33020..39908) overlaps with the start of sequence 282274.		
	Location/Qualifiers		
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	gene		
	CDS		

CP	5260	GCCCTTAAGGAGTACTGTATTCAAACCTCTGAAGCTGGATTTAACATCGATT	5201
Db	8159	TTTCAATTCTTCATTCTCGATTGTTAAAAAATCTAGAAAAAATGTTA	8218
Db	5200	TTTCAATTCTTCATTCTCGATTGTTAAAAAATCTGAAAAAATGTTA	5141
CP	5200	TTTCAATTCTTCATTCTCGATTGTTAAAAAATCTGAAAAAATGTTA	5141
Db	8219	TAACACTTCTAACTCTCATGATTTTCAATTGCAAAATAACRATCGGT	8278
Db	5140	TAACACTTCTAACTCTCATGATTTTCAATTGCAAAATAACRATCGGT	5081
CP	5080	TAACACTTCTAACTCTCATGATTTTCAATTGCAAAATAACRATCGGT	5021
DB	8339	TCTTTAAAGTTTAAAAATACATTCAATGAAACCCCTTGCACATTTCACAAT	8338
DB	5020	TCTTTAAAGTTTAAAAATACATTCAATGAAACCCCTTGCACATTTCACAAT	4961
CP	5020	TCTTTAAAGTTTAAAAATACATTCAATGAAACCCCTTGCACATTTCACAAT	4961
DB	8399	TTCATTGTCGATTGGATAATTGGAAATTTCAGAAAATGATTCTGTTATCAA	8458
CP	51960	TTCATTGTCGATTGGATAATTGGAAATTTCAGAAAATGATTCTGTTATCAA	4901
DB	8459	TTCATTGTCGATTGGATAATTGGAAATTTCAGAAAATGATTCTGTTATCAA	8518
CP	4900	TTCATTGTCGATTGGAAATTTCAGAAAATGATTCTGTTATCAA	4841
DB	8519	GAACAAACTAAAGAACATATGTAAGCAGGGAAAACGAAAATTCGAAACTAGGT	8578
CP	4840	GAACAAACTAAAGAACATATGTAAGCAGGGAAAACGAAAATTCGAAACTAGGT	4781
DB	8579	AATCATTTTCGCGGAAGTCAAAATTTCGACAGTGGCCATTAA	8638
CP	4780	AATCATTTTCGCGGAAGTCAAAATTTCGACAGTGGCCATTAA	4721
DB	8639	ACACAAATTGGCAAAATTGGCAAAATTATACATTTCGACAGTGGCCATTAA	8698
CP	4720	ACACAAATTGGCAAAATTTCGACAGTGGCCATTAA	4664
DB	8699	CGCGTTGGTATAATAATTTCGCGTACCTTCGGTCAGATGTCCTGCAAAATAACC	8758
CP	4663	CGCGTTGGTATAATAATTTCGCGTACCTTCGGTCAGATGTCCTGCAAAATAACC	4604
DB	8759	GTATACCCATGCACTGCAAAATTGGTAGATTCGCTTGCGCCATT	8818
CP	4603	GTATACCCATGCACTGCAAAATTGGTAGATTCGCTTGCGCCATT	4544
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CP	4543	CCTGTTGCATGTGCICAAGGTTTATTATGATGAGC	4501
RESULT	3	CEY6712	314495 bp DNA
DEFINITION		Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from	HTG
VERSION		Clone Y67H2, WORKING DRAFT SEQUENCE.	
ACCESSION			
NID	94469034		
AL022475.3	GI:4469034		
VERSION		HTG; HTGS_PHASE1.	
KEYWORDS		Caenorhabditis elegans.	
ORGANISM		Eukaryota; Metazoa; Nematoidea; Secernentea; Rhabditida;	
REFERENCE		Rhabditina; Rhabditidae; Rhabditida; Caenorhabditis.	
AUTHORS		(bases 1 to 314495)	
TITLE		McMurray,A.	
JOURNAL		Direct Submission	
		Submitted (04-MAR-1999) Nematode Sequencing Project, Sanger Centre,	
		Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,	
		Washington University, St. Louis, MO 63110, USA. E-mail:	
		jes@sanger.ac.uk or rwnematode.wustl.edu	
COMMENT		On Mar 22, 1999 this sequence version replaced gi:4468145. This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress	

and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES

Source
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
/clone="Y67H2"

BASE COUNT
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Query Match 93.6%; Score 936; DB 19; Length 314495;
Best Local Similarity 98.3%; Pred. 0.0e+00; Mismatches 0; Indels 7; Gaps 5;
Matches 988; Conservative 988; Mismatches 10; Indels 1; Gaps 5;

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Cp 5500 TTTCGGTTCTCTTGGATTTCGAGAAAATTGATTTTGGGTTGGACCAA 5441
Db 237575 AAACCAAAAAAAATCGAAATTGACTTTTGGATTAGGTTGGCTTTGAGAT 237634
Cp 5440 AAACCAAAAAAAATCGACTTTTGGATTAGGAAATTGACTTTTGGCTTTGAGAT 5381
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Cp 5380 TCAATTACTTTGGATTAGGAAATTGACTTTGGCAATTGGTC 5321
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Cp 5320 AAAACTACGTTACTGGTCTGACAGACAAATTGGTCATTGTC 5261
Db 237754 GCCTTAAGGAGTACTGTAATTCAAACTCTCGTTGGATTATTTTAAATCGAT 237813
Cp 5200 TTTCATTCCTTTCTCGATTGGTAAATTGAGATTGTTGGATTTAAATCGAT 5201
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Cp 5082 ATGAAATCTTTGAAATTGTGACGTTGGTTGATTTTGGGAGT 5023
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Db 238054 ATTTAAATTGGTCATTTCGAAATTTCGCTATTCGAAATTTCGCTATTC 238113
Cp 4962 ATTTAAATTGGTCATTTCGAAATTTCGCTATTCGAAATTTCGCTATTC 4903
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Cp 4902 AAGTTTGTATGGGAAATTGCTGAAATTTCGTTTACATCAAATA 4843
Db 238174 TAGAAAACAACTAGAAAACACATAATTAGCTGAAATTTCGAAACTPAG 238233
Cp 4842 TAGAAAACAACTAGAAAACACATAATTAGCTGAAACTPAG 4783
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